

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: HU, JING-SHAN  
ROSEN, CRAIG A.  
CAO, LIANG

(ii) TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA  
(F) ZIP: 20005

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED  
(B) FILING DATE: HERewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/207,550  
(B) FILING DATE: 8-MAR-1994  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/465,968  
(B) FILING DATE: 06-JUN-1995  
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED  
(B) FILING DATE: 24-DEC-1997  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 1488.1000003/EKS

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09935726-082401

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1674 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 12..80

- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 81..1268

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 12..1268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCCTTCAC C	ATG CAC TCG CTG GGC TTC TTC TCT GTG GCG TGT TCT CTG	50
Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu		
-23	-20 -15	
CTC GCC GCT GCG CTG CTC CCG GGT CCT CGC GAG GCG CCC GCC GCC GCC	98	
Leu Ala Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala		
-10 -5 1 5		
GCC GCC TTC GAG TCC GGA CTC GAC CTC TCG GAC GCG GAG CCC GAC GCG	146	
Ala Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala		
10 15 20		
GGC GAG GCC ACG GCT TAT GCA AGC AAA GAT CTG GAG GAG CAG TTA CGG	194	
Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg		
25 30 35		
TCT GTG TCC AGT GTA GAT GAA CTC ATG ACT GTA CTC TAC CCA GAA TAT	242	
Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr		
40 45 50		
TGG AAA ATG TAC AAG TGT CAG CTA AGG AAA GGA GGC TGG CAA CAT AAC	290	
Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn		
55 60 65 70		
AGA GAA CAG GCC AAC CTC AAC TCA AGG ACA GAA GAG ACT ATA AAA TTT	338	
Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe		
75 80 85		

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GCT GCA GCA CAT TAT AAT ACA GAG ATC TTG AAA AGT ATT GAT AAT GAG 386  
Ala Ala Ala His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu  
90 95 100

TGG AGA AAG ACT CAA TGC ATG CCA CGG GAG GTG TGT ATA GAT GTG GGG 434  
Trp Arg Lys Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly  
105 110 115

AAG GAG TTT GGA GTC GCG ACA AAC ACC TTC TTT AAA CCT CCA TGT GTG 482  
Lys Glu Phe Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val  
120 125 130

TCC GTC TAC AGA TGT GGG GGT TGC TGC AAT AGT GAG GGG CTG CAG TGC 530  
Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys  
135 140 145 150

ATG AAC ACC AGC ACG AGC TAC CTC AGC AAG ACG TTA TTT GAA ATT ACA 578  
Met Asn Thr Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr  
155 160 165

GTG CCT CTC TCT CAA GGC CCC AAA CCA GTA ACA ATC AGT TTT GCC AAT 626  
Val Pro Leu Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn  
170 175 180

CAC ACT TCC TGC CGA TGC ATG TCT AAA CTG GAT GTT TAC AGA CAA GTT 674  
His Thr Ser Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val  
185 190 195

CAT TCC ATT ATT AGA CGT TCC CTG CCA GCA ACA CTA CCA CAG TGT CAG 722  
His Ser Ile Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln  
200 205 210

GCA GCG AAC AAG ACC TGC CCC ACC AAT TAC ATG TGG AAT AAT CAC ATC 770  
Ala Ala Asn Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile  
215 220 225 230

TGC AGA TGC CTG GCT CAG GAA GAT TTT ATG TTT TCC TCG GAT GCT GGA 818  
Cys Arg Cys Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly  
235 240 245

GAT GAC TCA ACA GAT GGA TTC CAT GAC ATC TGT GGA CCA AAC AAG GAG 866  
Asp Asp Ser Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu  
250 255 260

CTG GAT GAA GAG ACC TGT CAG TGT GTC TGC AGA GCG GGG CTT CGG CCT 914  
Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro  
265 270 275

GCC AGC TGT GGA CCC CAC AAA GAA CTA GAC AGA AAC TCA TGC CAG TGT 962  
Ala Ser Cys Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys  
280 285 290

GTC TGT AAA AAC AAA CTC TTC CCC AGC CAA TGT GGG GCC AAC CGA GAA 1010  
Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu  
295 300 305 310

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TTT GAT GAA AAC ACA TGC CAG TGT GTA TGT AAA AGA ACC TGC CCC AGA 1058  
Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg  
315 320 325

AAT CAA CCC CTA AAT CCT GGA AAA TGT GCC TGT GAA TGT ACA GAA AGT 1106  
Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser  
330 335 340

CCA CAG AAA TGC TTG TTA AAA GGA AAG AAG TTC CAC CAC CAA ACA TGC 1154  
Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys  
345 350 355

AGC TGT TAC AGA CGG CCA TGT ACG AAC CGC CAG AAG GCT TGT GAG CCA 1202  
Ser Cys Tyr Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro  
360 365 370

GGA TTT TCA TAT AGT GAA GAA GTG TGT CGT TGT GTC CCT TCA TAT TGG 1250  
Gly Phe Ser Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp  
375 380 385 390

CAA AGA CCA CAA ATG AGC TAAGATTGTA CTGTTTTCCA GTTCATCGAT 1298  
Gln Arg Pro Gln Met Ser  
395

TTTCTATTAT GGAAACTGT GTTGCCACAG TAGAACTGTC TGTGAACAGA GAGACCCTTG 1358

TGGGTCCATG CTAACAAAGA CAAAAGTCTG TCTTTCTCTGA ACCATGTGGA TAACTTTACA 1418

GAAATGGACT GGAGCTCATC TGCAAAGGC CTCTTGTAAG GACTGTTTTT CTGCCAATGA 1478

CCAAACAGCC AAGATTTTCC TCTTGTGATT TCTTTAAAG AATGACTATA TAATTTATTT 1538

CCACTAAAAA TATTGTTTCT GCATTCATTT TTATAGCAAC AACAATTGGT AAAACTCACT 1598

GTGATCAATA TTTTATATC ATGCAAATA TGTTTAAAT AAAATGAAAA TTGTATTTAT 1658

AAAAAAAAA AAAAAA 1674

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 419 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala  
-23 -20 -15 -10

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe  
-5 1 5

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Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala  
 10 15 20 25

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser  
 30 35 40

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met  
 45 50 55

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln  
 60 65 70

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala  
 75 80 85

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys  
 90 95 100 105

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe  
 110 115 120

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr  
 125 130 135

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr  
 140 145 150

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu  
 155 160 165

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser  
 170 175 180 185

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile  
 190 195 200

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn  
 205 210 215

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys  
 220 225 230

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser  
 235 240 245

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu  
 250 255 260 265

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys  
 270 275 280

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys  
 285 290 295

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu

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300 305 310

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro  
315 320 325

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys  
330 335 340 345

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr  
350 355 360

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser  
365 370 375

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro  
380 385 390

Gln Met Ser  
395

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 71..142

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 143..1120

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 71..1120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGAGGCCACG GCTTATGCAA GCAAAGATCT GGAGGAGCAG TTACGGTCTG TGTCCAGTGT 60

AGATGAAGTC ATG ACT GTA CTC TAC CCA GAA TAT TGG AAA ATG TAC AAG 109

Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys

-24 -20 -15

TGT CAG CTA AGG AAA GGA GGC TGG CAA CAT AAC AGA GAA CAG GCC AAC 157

Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn

-10 -5 1 5

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CTC AAC TCA AGG ACA GAA GAG ACT ATA AAA TTT GCT GCA GCA CAT TAT Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr 10 15 20	205
AAT ACA GAG ATC TTG AAA AGT ATT GAT AAT GAG TGG AGA AAG ACT CAA Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln 25 30 35	253
TGC ATG CCA CGG GAG GTG TGT ATA GAT GTG GGG AAG GAG TTT GGA GTC Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val 40 45 50	301
GCG ACA AAC ACC TTC TTT AAA CCT CCA TGT GTG TCC GTC TAC AGA TGT Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys 55 60 65	349
GGG GGT TGC TGC AAT AGT GAG GGG CTG CAG TGC ATG AAC ACC AGC ACG Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr 70 75 80 85	397
AGC TAC CTC AGC AAG ACG TTA TTT GAA ATT ACA GTG CCT CTC TCT CAA Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln 90 95 100	445
GGC CCC AAA CCA GTA ACA ATC AGT TTT GCC AAT CAC ACT TCC TGC CGA Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg 105 110 115	493
TGC ATG TCT AAA CTG GAT GTT TAC AGA CAA GTT CAT TCC ATT ATT AGA Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg 120 125 130	541
CGT TCC CTG CCA GCA ACA CTA CCA CAG TGT CAG GCA GCG AAC AAG ACC Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr 135 140 145	589
TGC CCC ACC AAT TAC ATG TGG AAT AAT CAC ATC TGC AGA TGC CTG GCT Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala 150 155 160 165	637
CAG GAA GAT TTT ATG TTT TCC TCG GAT GCT GGA GAT GAC TCA ACA GAT Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp 170 175 180	685
GGA TTC CAT GAC ATC TGT GGA CCA AAC AAG GAG CTG GAT GAA GAG ACC Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr 185 190 195	733
TGT CAG TGT GTC TGC AGA GCG GGG CTT CGG CCT GCC AGC TGT GGA CCC Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro 200 205 210	781
CAC AAA GAA CTA GAC AGA AAC TCA TGC CAG TGT GTC TGT AAA AAC AAA His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys 215 220 225	829

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CTC TTC CCC AGC CAA TGT GGG GCC AAC CGA GAA TTT GAT GAA AAC ACA 877  
 Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr  
 230 235 240 245

TGC CAG TGT GTA TGT AAA AGA ACC TGC CCC AGA AAT CAA CCC CTA AAT 925  
 Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn  
 250 255 260

CCT GGA AAA TGT GCC TGT GAA TGT ACA GAA AGT CCA CAG AAA TGC TTG 973  
 Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu  
 265 270 275

TTA AAA GGA AAG AAG TTC CAC CAC CAA ACA TGC AGC TGT TAC AGA CGG 1021  
 Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg  
 280 285 290

CCA TGT ACG AAC CGC CAG AAG GCT TGT GAG CCA GGA TTT TCA TAT AGT 1069  
 Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser  
 295 300 305

GAA GAA GTG TGT CGT TGT GTC CCT TCA TAT TGG CAA AGA CCA CAA ATG 1117  
 Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro Gln Met  
 310 315 320 325

AGC TAAGATTGTA CTGTTTTCCTA GTTCATCGAT TTTCTATTAT GGAAACTGT 1170  
 Ser

GTTGCCACAG TAGAACTGTC TGTGAACAGA GAGACCCTTG TGGGTCCATG CTAACAAAGA 1230

CAAAAGTCTG TCTTTCCTGA ACCATGTGGA TAACTTTACA GAAATGGACT GGAGCTCATC 1290

TGCAAAAGGC CTCTGTAAA GACTGGTTTT CTGCCAATGA CCAAACAGCC AAGATTTTCC 1350

TCTTGTGATT TCTTTAAAAG AATGACTATA TAATTTATTT CCACTAAAAA TATTGTTTCT 1410

GCATTCATTT TTATAGCAAC AACAATTGGT AAAACTCACT GTGATCAATA TTTTATATC 1470

ATGCAAAATA TGTTTAAAAT AAAATGAAAA TTGTATTAT AAAAAAAAAA AAAAAA 1526

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 350 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys Cys Gln Leu  
 -24 -20 -15 -10

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Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn Leu Asn Ser  
-5 1 5

Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu  
10 15 20

Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro  
25 30 35 40

Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn  
45 50 55

Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys  
60 65 70

Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr Leu  
75 80 85

Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys  
90 95 100

Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser  
105 110 115 120

Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu  
125 130 135

Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro Thr  
140 145 150

Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala Gln Glu Asp  
155 160 165

Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp Gly Phe His  
170 175 180

Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr Cys Gln Cys  
185 190 195 200

Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro His Lys Glu  
205 210 215

Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe Pro  
220 225 230

Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys  
235 240 245

Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys  
250 255 260

Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu Leu Lys Gly  
265 270 275 280

Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Thr

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285 290 295

Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser Glu Glu Val  
300 305 310

Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro Gln Met Ser  
315 320 325

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala  
1 5 10 15

His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg  
20 25 30

Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu  
35 40 45

Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg  
50 55 60

Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu  
65 70 75 80

Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys  
85 90 95

Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro  
100 105 110

Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg  
115 120 125

Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg  
130 135 140

Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys  
145 150 155 160

Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu  
165 170 175

Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp

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180

185

190

Thr Asp Val Arg  
195

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 241 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg  
 1 5 10 15  
 Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met  
 20 25 30  
 Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu  
 35 40 45  
 His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met  
 50 55 60  
 Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg  
 65 70 75 80  
 Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu  
 85 90 95  
 Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp  
 100 105 110  
 Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln  
 115 120 125  
 Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr  
 130 135 140  
 Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg  
 145 150 155 160  
 Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu  
 165 170 175  
 Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser  
 180 185 190  
 Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val

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195                      200                      205

Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg  
 210                      215                      220

Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly  
 225                      230                      235                      240

Ala

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1                      5                      10                      15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20                      25                      30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35                      40                      45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50                      55                      60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65                      70                      75                      80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
 85                      90                      95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100                      105                      110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115                      120                      125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val  
 130                      135                      140

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr  
 145                      150                      155                      160

Lys Ser Trp Ser Val Tyr Val Gly Ala Arg Cys Cys Leu Met Pro Trp

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165 170 175  
 Ser Leu Pro Gly Pro His Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys  
 180 185 190  
 His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn  
 195 200 205  
 Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr  
 210 215 220  
 Cys Arg Cys Asp Lys Pro Arg Arg  
 225 230

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Pro Xaa Cys Val Xaa Xaa Xaa Arg Cys Xaa Gly Cys Cys Asn  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGCTTCCGG CTCGTATG

18

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGTTTTCCTCC AGTCACGAC

18

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCACATGGTT CAGGAAAGAC A

21

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGTAATACGA CTCACTATAG GGATCCCGCC ATGGAGGCCA CGGCTTATGC

50

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATCTCTAGA TTAGCTCATT TGTGGTCT

28

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCGGATCCA TGACTGTACT CTACCCA

27

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCTCTAGAT CAAGCGTAGT CTGGGACGTC GTATGGGTAC TCGAGGCTCA TTGTGGTCT

60

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3974 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCTT TTTTGAAT TCGTAATCAT  
 GGTCATAGCT GTTTCCTGTG TGAAATGTT ATCCGCTCAC AATCCACAC AACATACGAG  
 CCGGAAGCAT AAAGTGTAAG GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG  
 CGTTGCGCTC ACTGCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAATGAA  
 TCGGCCAACG CGCGGGGAGA GCGGTTTTCG GTATTGGGCG CTCTTCCGCT TCCTCGCTCA  
 CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG  
 TAATACGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAGGCC  
 AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTCCAT AGGCTCCGCC

60

120

180

240

300

360

420

480

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CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC	540
TATAAAGATA CCAGGCGTTT CCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC	600
TGCGGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA	660
GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTTC CTCCAAGCTG GGCTGTGTGC	720
ACGAACCCCC CGTTCAGCCC GACCGCTGCG CTTTATCCGG TAACTATCGT CTTGAGTCCA	780
ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG	840
CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGT GCCTAACTAC GGCTACACTA	900
GAAGAACAGT ATTTGGTATC TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG	960
GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC	1020
AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT	1080
CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCGTCGA	1140
CAATTCGCGC GCGAAGCGA AGCGGCATGC ATTTACGTTG ACACCATCGA ATGGTGCAAA	1200
ACCTTTCGCG GTATGGCATG ATAGCGCCCG GAAGAGAGTC AATTACGGGT GGTGAATGTG	1260
AAACCAGTAA CGTTATACGA TGTCGCAGAG TATGCCGGTG TCTCTTATCA GACCGTTTCC	1320
CGCGTGGTGA ACCAGGCCAG CCACGTTTCT GCGAAAACGC GGGAAAAAGT GGAAGCGGCG	1380
ATGGCGGAGC TGAATTACAT TCCCAACCGC GTGGCACAAC AACTGGCGGG CAAACAGTCG	1440
TTGCTGATTG GCGTTGCCAC CTCCAGTCTG GCCCTGCACG CGCCGTCGCA AATTGTGCGG	1500
GCGATTAAAT CTCGCGCCGA TCAACTGGGT GCCAGCGTGG TGGTGTGAT GGTAGAACGA	1560
AGCGGCGTCG AAGCCTGTAA AGCGGCGGTG CACAATCTTC TCGCGCAACG CGTCAGTGGG	1620
CTGATCATT ACTATCCGCT GGATGACCAG GATGCCATTG CTGTGGAAGC TGCCTGCACT	1680
AATGTTCCGG CGTTATTTCT TGATGTCTCT GACCAGACAC CCATCAACAG TATTATTTTC	1740
TCCCATGAAG ACGGTACGCG ACTGGGCGTG GAGCATCTGG TCGCATTGGG TCACCAGCAA	1800
ATCGCGCTGT TAGCGGGCCC ATTAAGTTCT GTCTCGGCGC GTCTGCGTCT GGCTGGCTGG	1860
CATAAATATC TCACTCGCAA TCAAATTCAG CCGATAGCGG AACGGGAAGG CGACTGGAGT	1920
GCCATGTCCG GTTTTCAACA AACCATGCAA ATGCTGAATG AGGGCATCGT TCCCACTGCG	1980
ATGCTGGTTG CCAACGATCA GATGGCGCTG GCGCAATGC GCGCCATTAC CGAGTCCGGG	2040
CTGCGCGTTG GTGCGGATAT CTCGGTAGTG GGATACGACG ATACCGAAGA CAGCTCATGT	2100
TATATCCCGC CGTTAACCAC CATCAAACAG GATTTTCGCC TGCTGGGGCA AACCAGCGTG	2160

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GACCGCTTGC TGCAACTCTC TCAGGGCCAG GCGGTGAAGG GCAATCAGCT GTTGCCCCGC	2220
TCACTGGTGA AAAGAAAAAC CACCCTGGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG	2280
TTGGCCGATT CATTAAATGCA GCTGGCACGA CAGGTTTCCC GACTGGAAAG CGGGCAGTGA	2340
GCGCAACGCA ATTAATGTAA GTTAGCGCGA ATTGTGACG AAAGCGGCCA TCGTGCCTCC	2400
CCACTCCTGC AGTTCGGGGG CATGGATGCG CGGATAGCGG CTGCTGGTTT CCTGGATGCC	2460
GACGGATTTG CACTGCGCGT AGAACTCCGC GAGGTCGTCC AGCCTCAGGC AGCAGCTGAA	2520
CCAACTCGCG AGGGGATCGA GCCCGGGGTG GCGAAGAAG TCCAGCATGA GATCCCCGCG	2580
CTGGAGGATC ATCCAGCCGG CGTCCCGGAA AACGATTCCG AAGCCCAACC TTTCATAGAA	2640
GGCGGCGGTG GAATCGAAAT CTCGTGATGG CAGGTTGGGC GTCGCTTGGT CGGTCATTTT	2700
GAACCCCAAG GTCCCGCTCA GAAGAACTCG TCAAGAAGGC GATAGAAGGC GATGCGCTGC	2760
GAATCGGGAG CGGCGATACC GTAAAGCAGC AGGAAGCGGT CAGCCCATTC GCCGCCAAGC	2820
TCTTCAGCAA TATCACGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC	2880
CGGCCACAGT CGATGAATCC AGAAAAGCG CCATTTTCCA CCATGATATT CGGCAAGCAG	2940
GCATCGCCAT GGGTCACGAC GAGATCCTCG CCGTCGGGCA TGCGCGCCTT GAGCCTGGCG	3000
AACAGTTCCG CTGGCGCGAG CCCCTGATGC TCTTCGTCCA GATCATCCTG ATCGACAAGA	3060
CCGGCTTCCA TCCGAGTACG TGCTCGCTCG ATGCGATGTT TCGCTTGGTG GTCGAATGGG	3120
CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC	3180
TCGGCAGGAG CAAGTGAGA TGACAGGAGA TCCTGCCCCG GCACTTCGCC CAATAGCAGC	3240
CAGTCCCTTC CCGCTTCAGT GACAACGTCG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG	3300
GCCAGCCACG ATAGCCGCGC TGCCTCGTCC TGCACTTCAT TCAGGGCACC GGACAGGTCG	3360
GTCTTGACAA AAAGAACCGG GCGCCCTGCG GCTGACAGCC GGAACACGGC GGCATCAGAG	3420
CAGCCGATTG TCTGTTGTGC CCAATCATAG CCGAATAGCC TCTCCACCCA AGCGGCCGGA	3480
GAACCTGCGT GCAATCCATC TTGTTCAATC ATGCGAAACG ATCCTCATCC TGTCTCTTGA	3540
TCAGATCTTG ATCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT	3600
TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTCGCTTGCT	3660
GTCCATAAAA CCGCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT	3720
CTCTTTGCGC TTGCGTTTTT CCTTGTCCAG ATAGCCAGT AGCTGACATT CATCCGGGGT	3780
CAGCACCGTT TCTGCGGACT GGCTTTCTAC GTGTTCCGCT TCCTTTAGCA GCCCTTGC	3840

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CCTGAGTGCT TCGGCAGCG TGAAGCTTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG 3900  
CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTTCACAC ATTAAAGAGG 3960  
AGAAATTACA TATG 3974

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 112 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AAGCTTAAAA AACTGCAAAA AATAGTTTGA CTTGTGAGCG GATAACAATT AAGATGTACC 60  
CAATTGTGAG CGGATAACAA TTTCACACAT TAAAGAGGAG AAATTACATA TG 112

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 419 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala  
1 5 10 15  
Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe  
20 25 30  
Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala  
35 40 45  
Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser  
50 55 60  
Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met  
65 70 75 80  
Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln  
85 90 95

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Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala  
100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys  
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe  
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr  
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr  
165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu  
180 185 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser  
195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile  
210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn  
225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys  
245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser  
260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu  
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys  
290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys  
305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu  
325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro  
340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys  
355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr  
370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser

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385

390

395

400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro  
405 410 415

Gln Met Ser

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCAGCACATA TGACAGAAGA GACTATAAAA

30

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCAGCAGGTA CCTCACAGTT TAGACATGCA

30

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAGCAGGTA CCTCAACGTC TAATAATGGA

30

(2) INFORMATION FOR SEQ ID NO:22:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCAGCAGGAT CCCACAGAAG AGACTATAAA

30

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCAGCATCTA GATCACAGTT TAGACATGCA

30

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCAGCAGGAT CCCACAGAAG AGACTATAAA ATTTGCTGC

39

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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GCAGCATCTA GATCAACGTC TAATAATGGA ATGAAC

36

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATCGATCCA TCATGCACTC GCTGGGCTTC TTCTCTGTGG CGTGTCTCTCT GCTCG

55

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCAGGGTACG GATCCTAGAT TAGCTCATTT GTGGTCTTT

39

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GACTGGATCC GCCACCATGC ACTCGCTGGG CTCTTCTC

39

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GACTGGTACC TTATCACATA AAATCTTCCT GAGCC

35

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GACTGGATCC GCCACCATGC ACTCGCTGGG CTTCTTCTC

39

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GACTGGTACC TTATCAGTCT AGTTCTTTGT GGGG

34

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GACTGGATCC GCCACCATGC ACTCGCTGGG CTTCTTCTC

39

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:

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104220-9275660

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACTGGTACC TCATTACTGT GGACTTTCTG TACATTC

37

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCAGCAGGAT CCACAGAAGA GACTATAAAA TTGCTGC

38

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGTCGTTCTA GATCACAGTT TAGACATGCA TCGGCAG

37

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